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Editorial

# Special issue: The Papillomavirus Episteme

Papillomaviruses are an ancient group of viruses that have coevolved along with their host species for millions of years; each virus is species specific and trophic for specific anatomical niches in the host epithelium. Papillomavirus infections can be asymptomatic, or can give rise to a wide range of pathologies, and a subset of papillomaviruses is strongly associated with human cancer. Unlike many other viruses, papillomaviruses are genetically stable and evolve at a slow rate along with the host. The availability of complete genome sequences from hundreds of different papillomaviruses provides a treasure trove of information for comparative genomics. This Special Issue is intended to be a companion resource to the Papillomavirus Episteme bioinformatics website (http://pave.niaid.nih.gov). The Papillomavirus Episteme hosts organized and curated information related to viral genomics. Each article in the Special Issue: Functional Genomics of Papillomaviruses provides an in-depth, unbiased and encyclopedic overview of different aspects of papillomavirus genomics and proteomics, written by experts in the papillomavirus field. Unlike other reviews, the main aim of each article is to completely document published details about each topic, so that this Special Issue will serve as an important reference resource for the scientific community.

Paul F. Lambert *
*University of Wisconsin School of Medicine and Public Health, 1400 University Ave, Madison, WI 53706, USA*
*E-mail address:* plambert@wisc.edu

Alison McBride
*National Institutes of Health, USA*

Hans Ulrich Bernard
*University of California, Irvine, USA*

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* Corresponding author. Tel.: +1 608 213 1196.

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